RAW SEQUENCE LISTING PATENT APPLICATION US/07/920,519

#18 DATE: 09/22/93 TIME: 09:25:53

	1			SEQUENCE LISTING	CMTC D CD
	2 3	(1) G	eneral Information:		ENTERED
	4				
	5	(i)	APPLICANT: CAPUT,		
	6			, PASCUAL	
	7			OT, JEAN-CLAUDE	
	8		KAGHAD,		
	9			RICHARD	
	10		LOISON,		
	11			ELIZABETH	
	12			JOHANNES	
	13			IS, PASCUAL	
	14 15		SALOME,	MARK	
	16	/::>	TITLE OF THURNTON	: URATE OXIDASE ACTIVITY	/ PROTEIN.
	17	(11)		E CODING THEREFOR, EXPRE	
	18			AND TRANSFORMED CELLS	,
	19		MICKO CKCMIDNO		
	20	(iii)	NUMBER OF SEQUENCE	s: 36	
	21	(/			
	22	(iv)	CORRESPONDENCE ADD	RESS:	
	23	` ,	(A) ADDRESSEE: Fo	ley & Lardner	
	24		(B) STREET: 1800	Diagonal Road, Suite 500	
	25		(C) CITY: Alexand	ria	
	26		(D) STATE: Virgin	ia	
	27		(E) COUNTRY: USA		
	28		(F) ZIP: 22313-02	99	
	29				
	30	(V)	COMPUTER READABLE		
	31		(A) MEDIUM TYPE:		
	32		(B) COMPUTER: IBM		
	33			TEM: PC-DOS/MS-DOS	1 //1 05
	34		(D) SOFTWARE: Pat	entIn Release #1.0, Vers	sion #1.25
	35		CURRENT ARRIVA	N DAMA	
	36	(AI)	CURRENT APPLICATIO		
-	37 38		(B) FILING DATE:	UMBER: US/07/920,519	
	39		(C) CLASSIFICATIO	N •	
	40		(C) CLASSIFICATIO	14 •	
	41	(vii)	PRIOR APPLICATION	ስልጥል •	
	42	(* 1 1)		UMBER: US/07/659,408	
	43		(B) FILING DATE:	0	
	44		(5) 1121110 511121		
	45	(viii)	ATTORNEY/AGENT INF	ORMATION:	
	46	` ,	(A) NAME: BENT, S		
	47		(B) REGISTRATION		
	48			KET NUMBER: 16781/276 BE	EDL
	49		•	•	
	50	(ix)	TELECOMMUNICATION	INFORMATION:	
	51		(A) TELEPHONE: (7	03)836-9300	

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DATE: 09/22/93 TIME: 09:25:59

52 53 54				LEFAX LEX:		703)6 149	683-4	109								
55 56	(2) INFO	RMATI	ON F	FOR S	SEQ I	D NO	0:1:									
57 58 59 60 61 62	(i)	(B)	LEN TYP	GTH:	: 301 amino	reris lami paci lines	ino a id		5							
63 64	(ii)	MOLE	CULE	TYP	PE: I	prote	ein									
65 66	(iii)	HYPO	THEI	CAI	L: NO)										
67 68 69	(vi)	ORIG (A)				: Aspei	rgil	lus 1	Elavu	ıs						
70 71 72 73	(vii)					E: ce ox	kidas	se								
74 75	(xi)	SEQU	ENCE	DES	CRII	OITS	N: SI	EQ II	NO:	1:						
76		Ala	Val	Lys		Ala	Arg	Tyr	Gly		Asp	Asn	Val	Arg	Val 15	Tyr
77 78	1				5					10					13	
79 80 81	Lys	Val 1	His	Lys 20	Asp	Glu	Lys	Thr	Gly 25	Val	Gln	Thr	Val	Tyr 30	Glu	Met
82 83	Thr	Val	Cys 35	Val	Leu	Leu	Glu	Gly 40	Glu	Ile	Glu	Thr	Ser 45	Tyr	Thr	Lys
84 85 86	Ala	Asp 5	Asn	Ser	Val	Ile	Val 55	Ala	Thr	Asp	Ser	Ile 60	Lys	Asn	Thr	Ile
87 88 89	Туг 65	Ile	Thr	Ala	Lys	Gln 70	Asn	Pro	Val	Thr	Pro 75	Pro	Glu	Leu	Phe	Gly 80
90 91 92	Ser	Ile	Leu	_	Thr 85					_			His		His 95	Ala
93 94 95	Ala	His	Val	Asn 100	Ile	Val	Cys	His	Arg 105	Trp	Thr	Arg	Met	Asp 110	Ile	Asp
96 97 98	Gly	Lys	Pro 115	His	Pro	His	Ser	Phe 120	Ile	Arg	Asp	Ser	Glu 125	Glu	Lys	Arg
99 100 101 102	Asn	Val (Gln	Val	Asp	Val	Val 135	Glu	Gly	Lys	Gly	Ile 140	Asp	Ile	Lys	Ser

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Ser Leu Ser Gly Leu Thr Val Leu Lys Ser Thr Asn Ser Gln Phe Trp 160 145 150 155 165 160 165 160 165					_							•	_	_			_
105				Ser	Gly	Leu		Val	Leu	Lys	Ser		Asn	Ser	GIn	Phe	
October Color Co		14:)				150					122					160
107		01 -	. Dh	7	B	7	01	m	mh	mb	T 011	T	C1	Th ₩	Trn) an	A = 0
108		GI	Pne	Leu	Arg		GIU	ryr	Int	Int		гÀа	GIU	THE	ırþ		ALG
11e						100					170					1/3	
110		т1.		802	mh.∽	7 00	Val	Agn	בות	Thr	Trn	Gln	Trn	T.v.c	Aan	Pho	Ser
111		116	: Leu	ser		nsp	vai	nap	ALG		111	GIII	пр	Dy 3		1 1	JCI
Cly Leu Gln Glu Val Arg Ser His Val Pro Lys Phe Asp Ala Thr Trp 113 195 200 205 205 114 115 Ala Thr Ala Arg Glu Val Thr Leu Lys Thr Phe Ala Glu Asp Asn Ser 210 215 220 225 220 225 220 225 226 225 235 240 120 225 230 240 120 225 235 240 120 225 235 240 120 225					100					103					170		
113		G1,	, T.O.1	Gln	Glu	Val	Ara	Ser	His	Val	Pro	Lvs	Phe	Asp	Ala	Thr	Trp
114 115		G.1.	Deu		Giu	A 17 T	9	001		,,,		-,-					
115				1,5													
116		Ala	Thr	Ala	Ara	Glu	Val	Thr	Leu	Lvs	Thr	Phe	Ala	Glu	Asp	Asn	Ser
117 118 Ala Ser Val Gln Ala Thr Met Tyr Lys Met Ala Glu Gln Ile Leu Ala 119 225 230 235 240 120 121 Arg Gln Gln Leu Ile Glu Thr Val Glu Tyr Ser Leu Pro Asn Lys His 122 245 250 255 123 124 Tyr Phe Glu Ile Asp Leu Ser Trp His Lys Gly Leu Gln Asn Thr Gly 125 260 265 270 126 127 Lys Asn Ala Glu Val Phe Ala Pro Gln Ser Asp Pro Asn Gly Leu Ile 128 275 129 130 Lys Cys Thr Val Gly Arg Ser Ser Leu Lys Ser Lys Leu 131 290 295 300 132 133 (2) INFORMATION FOR SEQ ID No:2: 134 (i) SEQUENCE CHARACTERISTICS: 136 (A) LENGTH: 302 amino acids 137 (B) TYPE: amino acid 138 (C) STRANDEDNESS: single 139 (D) TOPOLOGY: linear 140 141 (ii) MOLECULE TYPE: protein 142 143 (iii) HYPOTHETICAL: NO 144 145 (vi) ORIGINAL SOURCE: (A) ORGANISM: Aspergillus flavus 147 148 (vii) IMMEDIATE SOURCE: 149 (B) CLONE: Met-Urate oxidase 150 151 152 (xi) SEQUENCE DESCRIPTION: SEQ ID No:2:					9					-1-					•		
Ala Ser Val Gln Ala Thr Met Tyr Lys Met Ala Glu Gln Ile Leu Ala 119 225 230 235 240 240 240 240 240 241 240 241 245 245 255 255 255 255 245 250 255																	
119		Ala	Ser	Val	Gln	Ala	Thr	Met	Tvr	Lys	Met	Ala	Glu	Gln	Ile	Leu	Ala
120 121									•	•							
121																	
122		Arc	Gln	Gln	Leu	Ile	Glu	Thr	Val	Glu	Tyr	Ser	Leu	Pro	Asn	Lys	His
123 124		•															
Tyr Phe Glu Ile Asp Leu Ser Trp His Lys Gly Leu Gln Asn Thr Gly 125																	
125		Ty	Phe	Glu	Ile	Asp	Leu	Ser	Trp	His	Lys	Gly	Leu	Gln	Asn	Thr	Gly
Lys Asn Ala Glu Val Phe Ala Pro Gln Ser Asp Pro Asn Gly Leu Ile 275 280 285 129 130 Lys Cys Thr Val Gly Arg Ser Ser Leu Lys Ser Lys Leu 131 290 295 300 132 133 (2) INFORMATION FOR SEQ ID NO:2: 134 135 (i) SEQUENCE CHARACTERISTICS: 136 (A) LENGTH: 302 amino acids 137 (B) TYPE: amino acid 138 (C) STRANDEDNESS: single 139 (D) TOPOLOGY: linear 140 141 (ii) MOLECULE TYPE: protein 142 143 (iii) HYPOTHETICAL: NO 144 145 (vi) ORIGINAL SOURCE: 146 (A) ORGANISM: Aspergillus flavus 147 148 (vii) IMMEDIATE SOURCE: 149 (B) CLONE: Met-Urate oxidase 150 151 152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:		-				-			_		•	_					
128	126																
129 130	127	Ly	. Asn	Ala	Glu	Val	Phe	Ala	Pro	Gln	Ser	Asp	Pro	Asn	Gly	Leu	Ile
130	128			275					280					285			
131 290 295 300 132 133 (2) INFORMATION FOR SEQ ID NO:2: 134 135 (i) SEQUENCE CHARACTERISTICS: 136 (A) LENGTH: 302 amino acids 137 (B) TYPE: amino acid 138 (C) STRANDEDNESS: single 139 (D) TOPOLOGY: linear 140 141 (ii) MOLECULE TYPE: protein 142 143 (iii) HYPOTHETICAL: NO 144 145 (vi) ORIGINAL SOURCE: 146 (A) ORGANISM: Aspergillus flavus 147 148 (vii) IMMEDIATE SOURCE: 149 (B) CLONE: Met-Urate oxidase 150 151 152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	129																
132 133 (2) INFORMATION FOR SEQ ID NO:2: 134 135 (i) SEQUENCE CHARACTERISTICS: 136 (A) LENGTH: 302 amino acids 137 (B) TYPE: amino acid 138 (C) STRANDEDNESS: single 139 (D) TOPOLOGY: linear 140 141 (ii) MOLECULE TYPE: protein 142 143 (iii) HYPOTHETICAL: NO 144 145 (vi) ORIGINAL SOURCE: 146 (A) ORGANISM: Aspergillus flavus 147 148 (vii) IMMEDIATE SOURCE: 149 (B) CLONE: Met-Urate oxidase 150 151 152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	130	Ly	Cys	Thr	Val	Gly	Arg	Ser	Ser	Leu	Lys	Ser	Lys	Leu			
133 (2) INFORMATION FOR SEQ ID NO:2: 134 135 (i) SEQUENCE CHARACTERISTICS: 136 (A) LENGTH: 302 amino acids 137 (B) TYPE: amino acid 138 (C) STRANDEDNESS: single 139 (D) TOPOLOGY: linear 140 141 (ii) MOLECULE TYPE: protein 142 143 (iii) HYPOTHETICAL: NO 144 145 (vi) ORIGINAL SOURCE: 146 (A) ORGANISM: Aspergillus flavus 147 148 (vii) IMMEDIATE SOURCE: 149 (B) CLONE: Met-Urate oxidase 150 151 152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	131		290					295					300				
134 135 (i) SEQUENCE CHARACTERISTICS: 136 (A) LENGTH: 302 amino acids 137 (B) TYPE: amino acid 138 (C) STRANDEDNESS: single 139 (D) TOPOLOGY: linear 140 141 (ii) MOLECULE TYPE: protein 142 143 (iii) HYPOTHETICAL: NO 144 145 (vi) ORIGINAL SOURCE: 146 (A) ORGANISM: Aspergillus flavus 147 148 (vii) IMMEDIATE SOURCE: 149 (B) CLONE: Met-Urate oxidase 150 151 152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	132																
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 302 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (iii) HYPOTHETICAL: NO (vi) ORIGINAL SOURCE: (A) ORGANISM: Aspergillus flavus (vii) IMMEDIATE SOURCE: (B) CLONE: Met-Urate oxidase (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:		(2) INF	RMAT	ION :	FOR S	SEQ :	ID NO	0:2:									
(A) LENGTH: 302 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (iii) HYPOTHETICAL: NO (vi) ORIGINAL SOURCE: (A) ORGANISM: Aspergillus flavus (vii) IMMEDIATE SOURCE: (B) CLONE: Met-Urate oxidase (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:																	
137 (B) TYPE: amino acid 138 (C) STRANDEDNESS: single 139 (D) TOPOLOGY: linear 140 141 (ii) MOLECULE TYPE: protein 142 143 (iii) HYPOTHETICAL: NO 144 145 (vi) ORIGINAL SOURCE: 146 (A) ORGANISM: Aspergillus flavus 147 148 (vii) IMMEDIATE SOURCE: 149 (B) CLONE: Met-Urate oxidase 150 151 152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:		(i															
(C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (iii) HYPOTHETICAL: NO (vi) ORIGINAL SOURCE: (A) ORGANISM: Aspergillus flavus (vii) IMMEDIATE SOURCE: (B) CLONE: Met-Urate oxidase (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:			,	•					acid	5							
139 (D) TOPOLOGY: linear 140 141 (ii) MOLECULE TYPE: protein 142 143 (iii) HYPOTHETICAL: NO 144 145 (vi) ORIGINAL SOURCE: 146 (A) ORGANISM: Aspergillus flavus 147 148 (vii) IMMEDIATE SOURCE: 149 (B) CLONE: Met-Urate oxidase 150 151 152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:			•	•													
140 141 (ii) MOLECULE TYPE: protein 142 143 (iii) HYPOTHETICAL: NO 144 145 (vi) ORIGINAL SOURCE: 146 (A) ORGANISM: Aspergillus flavus 147 148 (vii) IMMEDIATE SOURCE: 149 (B) CLONE: Met-Urate oxidase 150 151 152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:									re								
141 (ii) MOLECULE TYPE: protein 142 143 (iii) HYPOTHETICAL: NO 144 145 (vi) ORIGINAL SOURCE: 146 (A) ORGANISM: Aspergillus flavus 147 148 (vii) IMMEDIATE SOURCE: 149 (B) CLONE: Met-Urate oxidase 150 151 152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:			(ט) TO.	POTO	iΥ: .	ıınea	ar									
142 143 (iii) HYPOTHETICAL: NO 144 145 (vi) ORIGINAL SOURCE: 146 (A) ORGANISM: Aspergillus flavus 147 148 (vii) IMMEDIATE SOURCE: 149 (B) CLONE: Met-Urate oxidase 150 151 152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:		, , , ,	WOT	D 0717	m mv:	nn											
143 (iii) HYPOTHETICAL: NO 144 145 (vi) ORIGINAL SOURCE: 146 (A) ORGANISM: Aspergillus flavus 147 148 (vii) IMMEDIATE SOURCE: 149 (B) CLONE: Met-Urate oxidase 150 151 152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:		(11	MOL	ECOL.	E TY	PE:]	prote	ein									
144 145 (vi) ORIGINAL SOURCE: 146 (A) ORGANISM: Aspergillus flavus 147 148 (vii) IMMEDIATE SOURCE: 149 (B) CLONE: Met-Urate oxidase 150 151 152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:		(333	מעם		י אר <i>י</i>	. NI	`										
145 (vi) ORIGINAL SOURCE: 146 (A) ORGANISM: Aspergillus flavus 147 148 (vii) IMMEDIATE SOURCE: 149 (B) CLONE: Met-Urate oxidase 150 151 152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:		(111	пір	OIUE	I I CA	P: 140	J										
146 (A) ORGANISM: Aspergillus flavus 147 148 (vii) IMMEDIATE SOURCE: 149 (B) CLONE: Met-Urate oxidase 150 151 152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:		155	OPT	CINA	ו פחו	ופכב											
147 148 (vii) IMMEDIATE SOURCE: 149 (B) CLONE: Met-Urate oxidase 150 151 152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:		(\ T						rail') 11 c ·	flavi	15						
148 (vii) IMMEDIATE SOURCE: 149 (B) CLONE: Met-Urate oxidase 150 151 152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:			(1)	, or	OTIT!	J. 1. 1	pe	911	_ u.ə								
149 (B) CLONE: Met-Urate oxidase 150 151 152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:		(vii	ТММ	EDTA	TE S	סנופכי	E:										
150 151 152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:		(* + + +						te o	xida	se							
151 152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:			, 2	, 55	· - ·			,		-							
152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:																	
· · · =		(xi	SEO	UENC	E DE	SCRI	PTIO	N: S	EQ I	ON O	:2:						
		,	~						_								

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154 155	Met 1	Ser	Ala	Val	Lys 5	Ala	Ala	Arg	Tyr	Gly 10	Lys	Asp	Asn	Val	Arg 15	Val
156 157 158	Tyr	Lys	Val	His 20	Lys	Asp	Glu	Lys	Thr 25	Gly	Val	Gln	Thr	Val 30	Tyr	Glu
159 160 161	Met	Thr	Val 35	Cys	Val	Leu	Leu	Glu 40	Gly	Glu	Ile	Glu	Thr 45	Ser	Tyr	Thr
162 163 164	Lys	Ala 50	Asp	Asn	Ser	Val	Ile 55	Val	Ala	Thr	Asp	Ser 60	Ile	Lys	Asn	Thr
165 166 167	Ile 65	Tyr	Ile	Thr	Ala	Lys 70	Gln	Asn	Pro	Val	Thr 75	Pro	Pro	Glu	Leu	Phe 80
168 169 170	Gly	Ser	Ile	Leu	Gly 85	Thr	His	Phe	Ile	Glu 90	Lys	Tyr	Asn	His	Ile 95	His
171 172 173	Ala	Ala	His	Val 100	Asn	Ile	Val	Cys	His 105	Arg	Trp	Thr	Arg	Met 110	Asp	Ile
174 175 176	Asp	Gly	Lys 115	Pro	His	Pro	His	Ser 120	Phe	Ile	Arg	Asp	Ser 125	Glu	Glu	Lys
177 178 179	Arg	Asn 130	Val	Gln	Val	Asp	Val 135	Val	Glu	Gly	Lys	Gly 140	Ile	Asp	Ile	Lys
180 181 182	Ser 145	Ser	Leu	Ser	Gly	Leu 150	Thr	Val	Leu	Lys	Ser 155	Thr	Asn	Ser	Gln	Phe 160
183 184 185	Trp	Gly	Phe	Leu	Arg 165	Asp	Glu	Tyr	Thr	Thr 170	Leu	Lys	Glu	Thr	Trp 175	Asp
186 187 188	Arg	Ile	Leu	Ser 180	Thr	Asp	Val	Asp	Ala 185	Thr	Trp	Gln	Trp	Lys 190	Asn	Phe
189 190 191	Ser	Gly	Leu 195	Gln	Glu	Val	Arg	Ser 200	His	Val	Pro	Lys	Phe 205	Asp	Ala	Thr
192 193 194	Trp	Ala 210	Thr	Ala	Arg	Glu	Val 215	Thr	Leu	Lys	Thr	Phe 220	Ala	Glu	Asp	Asn
195 196 197	Ser 225		Ser	Val	Gln	Ala 230	Thr	Met	Tyr	Lys	Met 235	Ala	Glu	Gln	Ile	Leu 240
198 199 200	Ala	Arg	Gln	Gln	Leu 245	Ile	Glu	Thr	Val	Glu 250	Tyr	Ser	Leu	Pro	Asn 255	Lys
201 202 203 204	His	Tyr	Phe	Glu 260	Ile	Asp	Leu	Ser	Trp 265	His	Lys	Gly	Leu	Gln 270	Asn	Thr

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205 206 207	Gly Lys Asn Ala Glu Val Phe Ala Pro Gln Ser Asp Pro Asn Gly Leu 275 280 285	
208 209 210	Ile Lys Cys Thr Val Gly Arg Ser Ser Leu Lys Ser Lys Leu 290 295 300	
211 212	(2) INFORMATION FOR SEQ ID NO:3:	
212	(i) SEQUENCE CHARACTERISTICS:	
214	(A) LENGTH: 906 base pairs	
215 216	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
217	(D) TOPOLOGY: linear	
218		
219	(ii) MOLECULE TYPE: DNA (genomic)	
220 221		
222	(vii) IMMEDIATE SOURCE:	
223	(B) CLONE: Preferred sequence for expression in	
224	prokaryotes	
225 226		
227	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
228	·	
229	ATGTCTGCGG TAAAAGCAGC GCGCTACGGC AAGGACAATG TTCGCGTCTA CAAGGTTCAC	60
230 231	AAGGACGAGA AGACCGGTGT CCAGACGGTG TACGAGATGA CCGTCTGTGT GCTTCTGGAG	120
231	ANGUNCONGN NUNCCOGIGI CONGNOGIG INCONGNIGN COGICIGIOI GOITOIGGIG	
233	GGTGAGATTG AGACCTCTTA CACCAAGGCC GACAACAGCG TCATTGTCGC AACCGACTCC	180
234		240
235 236	ATTAAGAACA CCATTTACAT CACCGCCAAG CAGAACCCCG TTACTCCTCC CGAGCTGTTC	240
237	GGCTCCATCC TGGGCACACA CTTCATTGAG AAGTACAACC ACATCCATGC CGCTCACGTC	300
238		
239	AACATTGTCT GCCACCGCTG GACCCGGATG GACATTGACG GCAAGCCACA CCCTCACTCC	360
240 241	TTCATCCGCG ACAGCGAGGA GAAGCGGAAT GTGCAGGTGG ACGTGGTCGA GGGCAAGGGC	420
241	TICHICCOCO ACAGCOAGGA GAAGCOGAAT GIGCAGGIGG ACGIGGICGA GGGCAAGGG	120
243	ATCGATATCA AGTCGTCTCT GTCCGGCCTG ACCGTGCTGA AGAGCACCAA CTCGCAGTTC	480
244		- 40
245	TGGGGCTTCC TGCGTGACGA GTACACCACA CTTAAGGAGA CCTGGGACCG TATCCTGAGC	540
246 247	ACCGACGTCG ATGCCACTTG GCAGTGGAAG AATTTCAGTG GACTCCAGGA GGTCCGCTCG	600
248		
249	CACGTGCCTA AGTTCGATGC TACCTGGGCC ACTGCTCGCG AGGTCACTCT GAAGACTTTT	660
250	GCTGAAGATA ACAGTGCCAG CGTGCAGGCC ACTATGTACA AGATGGCAGA GCAAATCCTG	720
251 252	GCIGAMGAIA ACAGIGCCAG CGIGCAGGCC ACIAIGIACA AGAIGGCAGA GCAAAICCIG	. 20
253	GCGCGCCAGC AGCTGATCGA GACTGTCGAG TACTCGTTGC CTAACAAGCA CTATTTCGAA	780
254		
255	ATCGACCTGA GCTGGCACAA GGGCCTCCAA AACACCGGCA AGAACGCCGA GGTCTTCGCT	840

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256		
257	CCTCAGTCGG ACCCCAACGG TCTGATCAAG TGTACCGTCG GCCGGTCCTC TCTGAAGTCT	900
258 259	AAATTG	906
260		
261	(2) INFORMATION FOR SEQ ID NO:4:	
262		
263	(i) SEQUENCE CHARACTERISTICS:	
264 265	(A) LENGTH: 906 base pairs (B) TYPE: nucleic acid	
266	(C) STRANDEDNESS: single	
267	(D) TOPOLOGY: linear	
268		
269	(ii) MOLECULE TYPE: DNA (genomic)	
270 271		
271	(vii) IMMEDIATE SOURCE:	
273	(B) CLONE: Preferred sequence for expression in	
274	eukaryotes	
275		
276	A LA CREATE PROCESSION OF TRANSPORT	
277 278	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
279	ATGTCTGCTG TTAAGGCTGC TAGATACGGT AAGGACAACG TTAGAGTCTA CAAGGTTCAC	60
280		
281	AAGGACGAGA AGACCGGTGT CCAGACGGTG TACGAGATGA CCGTCTGTGT GCTTCTGGAG	120
282		100
283	GGTGAGATTG AGACCTCTTA CACCAAGGCC GACAACAGCG TCATTGTCGC AACCGACTCC	180
284 285	ATTAAGAACA CCATTTACAT CACCGCCAAG CAGAACCCCG TTACTCCTCC CGAGCTGTTC	240
286	ATTAGAACA CONTITACAT CACCOCCIMO CACIMICOCCO TIMOTOCTOS COMOTETTO	
287	GGCTCCATCC TGGGCACACA CTTCATTGAG AAGTACAACC ACATCCATGC CGCTCACGTC	300
288		
289	AACATTGTCT GCCACCGCTG GACCCGGATG GACATTGACG GCAAGCCACA CCCTCACTCC	360
290 291	TTCATCCGCG ACAGCGAGGA GAAGCGGAAT GTGCAGGTGG ACGTGGTCGA GGGCAAGGGC	420
291	TICHICCOCO ACAGCOAGGA GAAGCOGAAT GIGCAGGIGG ACGIGGICGA GGGCAAGGGC	420
293	ATCGATATCA AGTCGTCTCT GTCCGGCCTG ACCGTGCTGA AGAGCACCAA CTCGCAGTTC	480
294		
295	TGGGGCTTCC TGCGTGACGA GTACACCACA CTTAAGGAGA CCTGGGACCG TATCCTGAGC	540
296	AGGARGAMAG AMAGARAMMA AGARMAGARA ARMMMARAMMA ARAMGARAGA COMOCOCOMOC	600
297 298	ACCGACGTCG ATGCCACTTG GCAGTGGAAG AATTTCAGTG GACTCCAGGA GGTCCGCTCG	000
299	CACGTGCCTA AGTTCGATGC TACCTGGGCC ACTGCTCGCG AGGTCACTCT GAAGACTTTT	660
300		
301	GCTGAAGATA ACAGTGCCAG CGTGCAGGCC ACTATGTACA AGATGGCAGA GCAAATCCTG	720
302	**************************************	700
303 304	GCGCGCCAGC AGCTGATCGA GACTGTCGAG TACTCGTTGC CTAACAAGCA CTATTTCGAA	780
304	ATCGACCTGA GCTGGCACAA GGGCCTCCAA AACACCGGCA AGAACGCCGA GGTCTTCGCT	840
306		

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DATE: 09/22/93 TIME: 09:26:39

307	CCTCAGTCGG ACCCCAACGG TCTGATCAAG TGTACCGTCG GCCGGTCCTC TCTGAAGTCT	900
308 309 310	AAATTG	906
311 312	(2) INFORMATION FOR SEQ ID NO:5:	
313 314 315 316 317 318	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
319 320	(ii) MOLECULE TYPE: DNA (genomic)	
321 322 323	(iii) HYPOTHETICAL: NO	
324 325 326 327 328	<pre>(vii) IMMEDIATE SOURCE: (B) CLONE: Preferred non-translated 5' sequence for</pre>	
329	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
330 331 332	AGCTTGCCGC CACT	14
333 334	(2) INFORMATION FOR SEQ ID NO:6:	
335 336 337 338 339 340	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 906 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
341 342	(ii) MOLECULE TYPE: DNA (genomic)	
343 344	(iii) HYPOTHETICAL: NO	
345 346 347 348 349 350	<pre>(vii) IMMEDIATE SOURCE: (B) CLONE: Preferred sequence for expression in animal</pre>	
351 352	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
353 354	ATGTCCGCAG TAAAAGCAGC CCGCTACGGC AAGGACAATG TCCGCGTCTA CAAGGTTCAC	60
355 356	AAGGACGAGA AGACCGGTGT CCAGACGGTG TACGAGATGA CCGTCTGTGT GCTTCTGGAG	120
357	GGTGAGATTG AGACCTCTTA CACCAAGGCC GACAACAGCG TCATTGTCGC AACCGACTCC	180

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358		240
359	ATTAAGAACA CCATTTACAT CACCGCCAAG CAGAACCCCG TTACTCCTCC CGAGCTGTTC	240
360 361	GGCTCCATCC TGGGCACACA CTTCATTGAG AAGTACAACC ACATCCATGC CGCTCACGTC	300
362	GGCTCCATCC TGGGCACACA CTTCATTGAG AAGTACAACC ACATCCATGC CGCTCACGTC	500
363	AACATTGTCT GCCACCGCTG GACCCGGATG GACATTGACG GCAAGCCACA CCCTCACTCC	360
364		
365	TTCATCCGCG ACAGCGAGGA GAAGCGGAAT GTGCAGGTGG ACGTGGTCGA GGGCAAGGGC	420
366		
367	ATCGATATCA AGTCGTCTCT GTCCGGCCTG ACCGTGCTGA AGAGCACCAA CTCGCAGTTC	480
368		
369	TGGGGCTTCC TGCGTGACGA GTACACCACA CTTAAGGAGA CCTGGGACCG TATCCTGAGC	540
370		600
371	ACCGACGTCG ATGCCACTTG GCAGTGGAAG AATTTCAGTG GACTCCAGGA GGTCCGCTCG	600
372	CARCAGO A COMO CARCA DA COMO CACA A COMO CACA A COMO A COMO CARCAGO CA	660
373	CACGTGCCTA AGTTCGATGC TACCTGGGCC ACTGCTCGCG AGGTCACTCT GAAGACTTTT	000
374 375	GCTGAAGATA ACAGTGCCAG CGTGCAGGCC ACTATGTACA AGATGGCAGA GCAAATCCTG	720
376	GCIGAAGAIA ACAGIGCCAG CGIGCAGGCC ACIAIGIACA MGAILGOACA GGILLLIGGIG	
377	GCGCGCCAGC AGCTGATCGA GACTGTCGAG TACTCGTTGC CTAACAAGCA CTATTTCGAA	780
378		
379	ATCGACCTGA GCTGGCACAA GGGCCTCCAA AACACCGGCA AGAACGCCGA GGTCTTCGCT	840
380		
381	CCTCAGTCGG ACCCCAACGG TCTGATCAAG TGTACCGTCG GCCGGTCCTC TCTGAAGTCT	900
382		
383	AAATTG	906
384		
385	(2) INFORMATION FOR SEQ ID NO:7:	
386 387	(i) SEQUENCE CHARACTERISTICS:	
388	(A) LENGTH: 23 base pairs	
389	(B) TYPE: nucleic acid	
390	(C) STRANDEDNESS: single	
391	(D) TOPOLOGY: linear	
392	(-)	
393	(ii) MOLECULE TYPE: DNA (genomic)	
394	· · ·	
395	(iii) HYPOTHETICAL: NO	
396		
397		
398	(vii) IMMEDIATE SOURCE:	
399	(B) CLONE: reverse transcription primer	
400		
401	() CEOURNOE DECODIREION, CEO ID NO.7.	
402 403	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
403	GATCCGGGCC CTTTTTTTT TTT	23
404		
406	(2) INFORMATION FOR SEQ ID NO:8:	
407		
408	(i) SEQUENCE CHARACTERISTICS:	

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409	(A) LENGTH: 10 amino acids
410	(B) TYPE: amino acid
411	(C) STRANDEDNESS: single
412	(D) TOPOLOGY: linear
413	• •
414	(ii) MOLECULE TYPE: peptide
415	. ,
416	(iii) HYPOTHETICAL: NO
417	()
418	
419	(vii) IMMEDIATE SOURCE:
420	(B) CLONE: Hydrolysis product T 17
421	(2) 220021 112 122 122 122
422	
423	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
424	(XI) DECORNOR DEBONITION. DEC 15 NO.0.
425	Asn Val Gln Val Asp Val Val Glu Gly Lys
425	1 5 10
427	1 3 10
427	(2) INFORMATION FOR SEQ ID NO:9:
429	(2) INFORMATION FOR SEQ ID NO. 3.
430	(i) SEQUENCE CHARACTERISTICS:
430	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 8 amino acids
432	(B) TYPE: amino acid
433	(C) STRANDEDNESS: single
434	(D) TOPOLOGY: linear
435	(11) NOT BOUT B. MUDD
436	(ii) MOLECULE TYPE: peptide
437	(
438	(iii) HYPOTHETICAL: NO
439	
440	A LLA TAMENTARE CONDER
441	(vii) IMMEDIATE SOURCE:
442	(B) CLONE: Hydrolysis product T 20
443	
444	
445	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
446	
447	Asn Phe Ser Gly Leu Gln Glu Val
448	1 5
449	
450	(2) INFORMATION FOR SEQ ID NO:10:
451	
452	(i) SEQUENCE CHARACTERISTICS:
453	(A) LENGTH: 6 amino acids
454	(B) TYPE: amino acid
455	(C) STRANDEDNESS: single
456	(D) TOPOLOGY: linear
457	
458	(ii) MOLECULE TYPE: peptide
459	

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```
460
         (iii) HYPOTHETICAL: NO
461
462
463
         (vii) IMMEDIATE SOURCE:
464
                (B) CLONE: Hydrolysis product T 23
465
466
467
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
468
469
           Phe Asp Ala Thr Trp Ala
470
471
      (2) INFORMATION FOR SEQ ID NO:11:
472
473
           (i) SEQUENCE CHARACTERISTICS:
474
475
                (A) LENGTH: 8 amino acids
476
                (B) TYPE: amino acid
477
                (C) STRANDEDNESS: single
478
                (D) TOPOLOGY: linear
479
          (ii) MOLECULE TYPE: peptide
480
481
482
         (iii) HYPOTHETICAL: NO
483
484
485
         (vii) IMMEDIATE SOURCE:
486
                (B) CLONE: Hydrolysis product T 27
487
488
489
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
490
491
           His Tyr Phe Glu Ile Asp Leu Ser
492
           1
                            5
493
494
      (2) INFORMATION FOR SEQ ID NO:12:
495
496
           (i) SEQUENCE CHARACTERISTICS:
497
                (A) LENGTH: 13 amino acids
498
                (B) TYPE: amino acid
499
                (C) STRANDEDNESS: single
500
                (D) TOPOLOGY: linear
501
502
          (ii) MOLECULE TYPE: peptide
503
         (iii) HYPOTHETICAL: NO
504
505
506
507
         (vii) IMMEDIATE SOURCE:
508
                (B) CLONE: Hydrolysis product T 28
509
510
```

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```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
511
512
513
           Ile Leu Ser Thr Asp Val Asp Ala Thr Trp Gln Trp Lys
514
           1
515
     (2) INFORMATION FOR SEQ ID NO:13:
516
517
           (i) SEQUENCE CHARACTERISTICS:
518
519
                (A) LENGTH: 11 amino acids
520
                (B) TYPE: amino acid
                (C) STRANDEDNESS: single
521
522
                (D) TOPOLOGY: linear
523
          (ii) MOLECULE TYPE: peptide
524
525
         (iii) HYPOTHETICAL: NO
526
527
528
529
         (vii) IMMEDIATE SOURCE:
530
                (B) CLONE: Hydrolysis product T 29
531
532
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
533
534
535
          His Tyr Phe Glu Ile Asp Leu Ser Trp His Lys
536
537
      (2) INFORMATION FOR SEQ ID NO:14:
538
539
540
           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 11 amino acids
541
542
                (B) TYPE: amino acid
                (C) STRANDEDNESS: single
543
544
                (D) TOPOLOGY: linear
545
546
          (ii) MOLECULE TYPE: peptide
547
548
         (iii) HYPOTHETICAL: NO
549
550
         (vii) IMMEDIATE SOURCE:
551
                (B) CLONE: Hydrolysis product T 31
552
553
554
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
555
556
557
           Ser Thr Asn Ser Gln Phe Trp Gly Phe Leu Arg
558
559
560
      (2) INFORMATION FOR SEQ ID NO:15:
561
```

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562 563 564 565 566 567	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
568 569	(ii)	MOLECULE TYPE: peptide
570 571 572	(iii)	HYPOTHETICAL: NO
573 574 575 576	(vii)	IMMEDIATE SOURCE: (B) CLONE: Hydrolysis product T 32
577 578	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:15:
579 580 581 582	Gln 1	Asn Pro Val Thr Pro Pro Glu Leu Phe Gly Ser Ile Leu Gly Thr 5 10 15
583 584	(2) INFO	RMATION FOR SEQ ID NO:16:
585 586 587 588 589 590	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
591 592	(ii)	MOLECULE TYPE: peptide
593 594 595	(iii)	HYPOTHETICAL: NO
596 597 598 599	(vii)	IMMEDIATE SOURCE: (B) CLONE: Hydrolysis product T 33
600 601		SEQUENCE DESCRIPTION: SEQ ID NO:16:
602 603 604 605	Gln 1	Asn Pro Val Thr Pro Pro Glu Leu Phe Gly Ser Ile Leu Gly Thr 5 10 15
606 607	(2) INFO	RMATION FOR SEQ ID NO:17:
608 609 610 611 612	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

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613		
614	(;;)	MOLECULE TYPE: peptide
615	(11)	MODECOLD IIIL. Poperac
616	(1111)	HYPOTHETICAL: NO
617	(111)	MITOINDIIOND. NO
618		
619	(vii)	IMMEDIATE SOURCE:
620	(* 1 1)	(B) CLONE: Hydrolysis product V 1
621		(b) Chomb. Mydrorysis produce v r
622		
623	(vi)	SEQUENCE DESCRIPTION: SEQ ID NO:17:
624	(XI)	DECORNOR DEBONITION. DEC 15 NO.17.
625	Tur	Ser Leu Pro Asn Lys His Tyr Phe Glu Ile Asp Leu Ser Trp His
626	1	5 10 15
627	1	J 10 15
628	Two	
629	Lys	
630		
631	(2) TNEO	RMATION FOR SEQ ID NO:18:
632	(2) INFO	AMATION FOR SEQ ID NO.10.
633	/33	SEQUENCE CHARACTERISTICS:
634	(+)	(A) LENGTH: 16 amino acids
635		(B) TYPE: amino acid
636		(C) STRANDEDNESS: single
637		(D) TOPOLOGY: linear
638		(b) TOPOLOGI: Illiear
639	1333	MOLECULE TYPE: peptide
640	(11)	MODECOLE IIIE. pepcide
641	(:::)	HYPOTHETICAL: NO
642	(111)	nifolitations. No
643		
644	/ : : \	IMMEDIATE SOURCE:
645	(\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	(B) CLONE: Hydrolysis product V 2
646		(b) Chore: hydrolysis produce v z
647		
648	(**)	SEQUENCE DESCRIPTION: SEQ ID NO:18:
649	(XI)	DECORAGE DESCRIPTION. DEC ID NO.10.
650	1/a1	Thr Leu Lys Thr Phe Ala Glu Asp Asn Ser Ala Ser Val Gln Ala
651	1	5 10 15
652	1	5 10 13
653		
654	(2) TNEO	RMATION FOR SEQ ID NO:19:
655	(Z) INFO	dention for one in no.1).
656	/ ;)	SEQUENCE CHARACTERISTICS:
657	(+)	(A) LENGTH: 24 amino acids
658		(B) TYPE: amino acid
659		(C) STRANDEDNESS: single
660		(D) TOPOLOGY: linear
661		(b) Totoboot, Itheat
662	(111	MOLECULE TYPE: peptide
663	(+ +)	MODBOODD IIIB. Pepcide
000		

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664 665	(iii)	HYPOTHETICAL: NO
666 667 668 669 670	(vii)	IMMEDIATE SOURCE: (B) CLONE: Hydrolysis product V 3
671 672	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:19:
673	Thr	Ser Tyr Thr Lys Ala Asp Asn Ser Val Ile Val Asp Thr Asp Ser
674	1	5 10 15
675		
676	Ile	Lys Asn Thr Ile Tyr Ile Thr
677		20
678		
679	(2) TNFO	RMATION FOR SEQ ID NO:20:
680	(2) 111101	Manifold Tolk Bbg 15 Hollot
681	(1)	SEQUENCE CHARACTERISTICS:
682	(-)	(A) LENGTH: 28 amino acids
683		(B) TYPE: amino acid
684		(C) STRANDEDNESS: single
685		(D) TOPOLOGY: linear
686		(b) TOPOLOGI: Timedi
	1111	NOT ECHIE WARE montide
687	(11)	MOLECULE TYPE: peptide
688		THE DOMESTICAL INC.
689	(111)	HYPOTHETICAL: NO
690		
691		
692	(A11)	IMMEDIATE SOURCE:
693		(B) CLONE: Hydrolysis product V 5
694		
695	4 4 .	CROHENCE DECORIDATION, CRO ID NO.20.
696 697	(XI)	SEQUENCE DESCRIPTION: SEQ ID NO:20:
69 <i>1</i>	G1	Lys Gly Ile Asp Ile Lys Ser Ser Leu Ser Gly Leu Thr Val Leu
699		
700	1	5 10 15
	7	Con The Act Con Cla Pho Ten Cla Pho Lou Ara
701	rys	Ser Thr Asn Ser Gln Phe Trp Gly Phe Leu Arg 20 25
702		20 25
703		
704	(2) INFO	RMATION FOR SEQ ID NO:21:
705		
706	(i)	SEQUENCE CHARACTERISTICS:
707		(A) LENGTH: 17 amino acids
708		(B) TYPE: amino acid
709		(C) STRANDEDNESS: single
710		(D) TOPOLOGY: linear
711		
712	(ii)	MOLECULE TYPE: peptide
713		
714	(iii)	HYPOTHETICAL: NO

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715			
716			
717	(vii)	IMMEDIATE SOURCE:	
718		(B) CLONE: Hydolysis product V 6	
719			
720			
721	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:21:	
722			
723	Gly	Lys Gly Ile Asp Ile Lys Ser Ser Leu Ser Gly Leu Thr Val Leu	
724	1	5 10 15	
725			
726	Lys		
727	•		
728			
729	(2) INFO	RMATION FOR SEQ ID NO:22:	
730	` '	-	
731	(i)	SEQUENCE CHARACTERISTICS:	
732	(-)	(A) LENGTH: 1236 base pairs	
733		(B) TYPE: nucleic acid	
734		(C) STRANDEDNESS: single	
735		(D) TOPOLOGY: linear	
736		(5) 20102001 2211002	
737	(ii)	MOLECULE TYPE: DNA (genomic)	
738	()		
739	(iii)	HYPOTHETICAL: NO	
740	(,		
741			
742	(vii)	IMMEDIATE SOURCE:	
743	(/	(B) CLONE: Fragment 3	
744		(=, ===================================	
745			
746	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:22:	
747	(/		
748	GATCCGCG	GA AGCATAAAGT GTAAAGCCTG GGGTGCCTAA TGAGTGAGCT AACTTACATT	60
749			
750	AATTGCGT	TG CGCTCACTGC CCGCTTTCCA GTCGGGAAAC CTGTCGTGCC AGCTGCATTA	120
751			
752	ATGAATCG	GC CAACGCGCGG GGAGAGGCGG TTTGCGTATT GGGCGCCAGG GTGGTTTTTC	180
753			
754	TTTTCACC	AG TGAGACGGGC AACAGCTGAT TGCCCTTCAC CGCCTGGCCC TGAGAGAGTT	240
755			
756	GCAGCAAG	CG GTCCACGCTG GTTTGCCCCA CCACCCGAAA ATCCTGTTTG ATGGTGGTTA	300
757			
758	ACGGCGGG	AT ATAACATGAG CTGTCTTCGG TATCGTCGTA TCCCACTACC GAGATATCCG	360
759			
760	CACCAACG	CG CAGCCCGGAC TCGGTAATGG CGCGCATTGC GCCCAGCGCC ATCTGATCGT	420
761	3		. — •
762	TGGCAACC	AG CATCGCAGTG GGAACGATGC CCTCATTCAG CATTTGCATG GTTTGTTGAA	480
763			
764	AACCGGAC	AT GGCACTCCAG TCGCCTTCCC GTTCCGCTAT CGGCTGAATT TGATTGCGAG	540
765			

816

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766	TGAGATATTT ATGCCAGCCA GCCAGACGCA GACGCGCCGA GACAGAACTT AATGGGCCCG	600
767 768	CTAACAGCGC GATTTGCTGG TGACCCAATG CGACCAGATG CTCCACGCCC AGTCGCGTAC	660
769 770 771	CGTCTTCATG GGAGAAAATA ATACTGTTGA TGGGTGTCTG GTCAGAGACA TCAAGAAATA	720
771 772 773	ACGCCGGAAC ATTAGTGCAG GCAGCTTCCA CAGCAATGGC ATCCTGGTCA TCCAGCGGAT	780
774 775	AGTTAATGAT CAGCCCACTG ACGCGTTGCG CGAGAAGATT GTGCACCGCC GCTTTACAGG	840
776 777	CTTCGACGCC GCTTCGTTCT ACCATCGACA CCACCACGCT GGCACCCAGT TGATCGGCGC	900
778 779	GAGATTTAAT CGCCGCGACA ATTTGCGACG GCGCGTGCAG GGCCAGACTG GAGGTGGCAA	960
780 781	CGCCAATCAG CAACGACTGT TTGCCCGCCA GTTGTTGTGC CACGCGGTTG GGAATGTAAT	1020
782 783	TCAGCTCCGC CATCGCCGCT TCCACTTTTT CCCGCGTTTT CGCAGAAACG TGGCTGGCCT	1080
784 785	GGTTCACCAC GCGGGAAACG GTCTGATAAC AGACACCGGC ATACTCTGCG ACATCGTATA	1140
786 787	ACGTTACTGG TTTCACATTC ACCACCCTGA ATTGACTCTC TTCCGGGCGC TATCATGCCA	1200
788 789	TACCGCGAAA GGTTTTGCGC CATTCGATGG TGTCCG	1236
790 791	(2) INFORMATION FOR SEQ ID NO:23:	
792	(i) SEQUENCE CHARACTERISTICS:	
793 794	(A) LENGTH: 321 base pairs	
794 795	(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
796	(D) TOPOLOGY: linear	
797	(0) 10102011 220011	
798	(ii) MOLECULE TYPE: DNA (genomic)	
799		
800	(iii) HYPOTHETICAL: NO	
801 802		
803	(vii) IMMEDIATE SOURCE:	
804	(B) CLONE: Fragment 4	
805	(2) 020.21 1249	
806	(ix) FEATURE:	
807	(A) NAME/KEY: CDS	
808	(B) LOCATION: 107316	
809	(D) OTHER INFORMATION: /product= "regulatory signal + aa	
810	1-44 human growth hormone precursor"	
811		
812 813	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
814	(VI) PEGORNOR DESCRIPTION. PEG ID MO:53:	
815	TCGAGCTGAC TGACCTGTTG CTTATATTAC ATCGATAGCG TATAATGTGT GGAATTGTGA	60
816		

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817 818 819 820	GCG	ATAA	CAA :	rttc?	ACAC	AG T	CTAA(CTTT	A AG	AAGG?	AGAT	ATA		ATG (Met 1	_		115
821 822 823			CGG Arg														163
824 825 826 827			CAA Gln														211
828 829 830 831			AAC Asn														259
832 833 834 835			TAC Tyr														307
836 837 838 839 840			TTC Phe 70		CA												321
841 842 843 844 845 846	(2)		ORMA:	SEQUI (A)		CHAI	RACTI	ERIS'	TICS no a								
847 848 849		(ii) 1	(D)	TOI	POLO	GY: :	line	ar								
850 851		•	, . xi) :				-			Q ID	NO:	24:					
852 853 854 855	Met 1	Ala	Thr	Gly	Ser 5	Arg	Thr	Ser	Leu	Leu 10	Leu	Ala	Phe	Gly	Leu 15	Leu	
856 857 858	Cys	Leu	Pro	Trp 20	Leu	Gln	Glu	Gly	Ser 25	Ala	Phe	Pro	Thr	Ile 30		Leu	
859 860 861	Ser	Arg	Leu 35	Phe	Asp	Asn	Ala	Met 40	Leu	Arg	Ala	His	Arg 45	Leu	His	Gln	
862 863 864	Leu	Ala 50	Phe	Asp	Thr	Tyr	Gln 55	Glu	Phe	Glu	Glu	Ala 60	Tyr	Ile	Pro	Lys	
865 866 867	Glu 65	Gln	Lys	Tyr	Ser	Phe 70											

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868 869	(2) INFORMATION FOR SEQ ID NO:25:	
870	(i) SEQUENCE CHARACTERISTICS:	
871	(A) LENGTH: 74 base pairs	
872	(B) TYPE: nucleic acid	
873	(C) STRANDEDNESS: double	
874	(D) TOPOLOGY: linear	
875	(b) Totoboot. Timed	
876	(ii) MOLECULE TYPE: DNA (genomic)	
877	(II) Modbooth IIII. Dim (genemic)	
878	(iii) HYPOTHETICAL: NO	
879	(III) MIGHERICAE. NO	
880		
881	(vii) IMMEDIATE SOURCE:	
882	(VII) TAMEDIATE SOCKES. (B) CLONE: ClaI-NdeI fragment	
883	(b) Chors. Clai-well flagment	
884		
885	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
886	(XI) SEQUENCE DESCRIPTION: SEQ ID NO.23:	
887	CGATAGCGTA TAATGTGTGG AATTGTGAGC GGATAACAAT TTCACACAGT TTTTCGCGAA	60
888	CONTROCOTA TANIGIGIOS ANTIGIONOS CONTRACAMI TICNONOMOI TITTOCOCA.	
889	GAAGGAGATA TACA	74
890	emodedata thos	
891	(2) INFORMATION FOR SEQ ID NO:26:	
892	(2) INFORMATION TON BEG ID NO.20.	
893	(i) SEQUENCE CHARACTERISTICS:	
894	(A) LENGTH: 190 base pairs	
895	(B) TYPE: nucleic acid	
896	(C) STRANDEDNESS: double	
897	(D) TOPOLOGY: linear	
898	(b) Totaleatt Timed	
899	(ii) MOLECULE TYPE: DNA (genomic)	
900	(II) London IIII. Dim (genemia)	
901	(iii) HYPOTHETICAL: NO	
902	(III) III o	
903		
904	(vii) IMMEDIATE SOURCE:	
905	(B) CLONE: Plasmid p373,2 fragment	
906	(b) obother readment por one readment	
907		
908	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
909	(112, 122, 113, 113, 113, 113, 113, 113,	
910	GATCTTCAAG CAGACCTACA GCAAGTTCGA CACAAACTCA CACAACGATG ACGCACTACT	60
911		
912	CAAGAACTAC GGGCTGCTCT ACTGCTTCAG GAAGGACATG GACAAGGTCG AGACATTCCT	120
913		
914	GCGCATCGTG CAGTGCCGCT CTGTGGAGGG CAGCTGTGGC TTCTAGTAAG GTACCCTGCC	180
915	didinitiii dhaladaa dididahaa dhaaladaa lidhaalaa dhaadaa	
916	CTACGTACCA	190
917	V1.10V1.10V1.	
918	(2) INFORMATION FOR SEQ ID NO:27:	
	\-\	

RAW SEQUENCE LISTING PATENT APPLICATION US/07/920,519

DATE: 09/22/93 TIME: 09:28:15

919		
920	(i) SEQUENCE CHARACTERISTICS:	
921	(A) LENGTH: 48 base pairs	
922	(B) TYPE: nucleic acid	
923	(C) STRANDEDNESS: single	
924	(D) TOPOLOGY: linear	
925		
926	(ii) MOLECULE TYPE: DNA (genomic)	
927	(3	
928	(iii) HYPOTHETICAL: NO	
929	(600, 10000000000000000000000000000000000	
930		
931	(vii) IMMEDIATE SOURCE:	
932	(B) CLONE: AccI-NdeI synthetic fragment	
933	(b) Cloud. Heel had symmetry linguistry	
934		
935	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:	
936	(XI) SEQUENCE DESCRIPTION. SEQ ID NO.27.	
	TANGER OF THE PROPERTY OF THE	48
937	TATGTCTGCG GTAAAAGCAG CGCGCTACGG CAAGGACAAT GTTCGCGT	40
938	(A) TUPOPUNTON FOR CTO IN NO. 20.	
939	(2) INFORMATION FOR SEQ ID NO:28:	
940	All Charles and Carles	
941	(i) SEQUENCE CHARACTERISTICS:	
942	(A) LENGTH: 360 base pairs	
943	(B) TYPE: nucleic acid	
944	(C) STRANDEDNESS: single	
945	(D) TOPOLOGY: linear	
946		
947	(ii) MOLECULE TYPE: DNA (genomic)	
948		
949	(iii) HYPOTHETICAL: NO	
950		
951		
952	(vii) IMMEDIATE SOURCE:	
953	(B) CLONE: Plasmid pEMR469 fragment	
954		
955		
956	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:	
957		
958	GGGACGCGTC TCCTCTGCCG GAACACCGGG CATCTCCAAC TTATAAGTTG GAGAAATAAG	60
959		
960	AGAATTTCAG ATTGAGAGAA TGAAAAAAAA AAAAAAAAAA	120
961		
962	AATGGGGTTC ACTTTTTGGT AAAGCTATAG CATGCCTATC ACATATAAAT AGAGTGCCAG	180
963		
964	TAGCGACTTT TTTCACACTC GAGATACTCT TACTACTGCT CTCTTGTTGT TTTTATCACT	240
965		
966	TCTTGTTTCT TCTTGGTAAA TAGAATATCA AGCTACAAAA AGCATACAAT CAACTATCAA	300
967		
968	CTATTAACTA TATCGATACC ATATGGATCC GTCGACTCTA GAGGATCGTC GACTCTAGAG	360
969		
709		

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970 971	(2) INFORMATION FOR SEQ ID NO:29:	
972 973 974 975 976 977 978	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 58 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
979 980	(ii) MOLECULE TYPE: DNA (genomic)	
981 982 983	(iii) HYPOTHETICAL: NO	
984 985 986 987	<pre>(vii) IMMEDIATE SOURCE: (B) CLONE: Fragment C</pre>	
988 989	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
990 991	CGATATACAC AATGTCTGCT GTTAAGGCTG CTAGATACGG TAAGGACAAC GTTAGAGT	58
992 993	(2) INFORMATION FOR SEQ ID NO:30:	
994 995 996 997 998 999	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1013 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
1000 1001	(ii) MOLECULE TYPE: DNA (genomic)	
1002 1003 1004	(iii) HYPOTHETICAL: NO	
1005 1006 1007 1008	<pre>(vii) IMMEDIATE SOURCE: (B) CLONE: Fragment D</pre>	
1009 1010	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
1011 1012	CTACAAGGTT CACAAGGACG AGAAGACCGG TGTCCAGACG GTGTACGAGA TGACCGTCTG	60
1013 1014	TGTGCTTCTG GAGGGTGAGA TTGAGACCTC TTACACCAAG GCCGACAACA GCGTCATTGT	120
1015 1016	CGCAACCGAC TCCATTAAGA ACACCATTTA CATCACCGCC AAGCAGAACC CCGTTACTCC	180
1017 1018	TCCCGAGCTG TTCGGCTCCA TCCTGGGCAC ACACTTCATT GAGAAGTACA ACCACATCCA	240
1019 1020	TGCCGCTCAC GTCAACATTG TCTGCCACCG CTGGACCCGG ATGGACATTG ACGGCAAGCC	300

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DATE: 09/22/93 TIME: 09:28:31

1021	ACACCCTCAC TCCTTCATCC GCGACAGCGA GGAGAAGCGG AATGTGCAGG TGGACGTGGT	360
1022 1023	CGAGGGCAAG GGCATCGATA TCAAGTCGTC TCTGTCCGGC CTGACCGTGC TGAAGAGCAC	420
1024		
1025 1026	CAACTCGCAG TTCTGGGGCT TCCTGCGTGA CGAGTACACC ACACTTAAGG AGACCTGGGA	480
1026	CCGTATCCTG AGCACCGACG TCGATGCCAC TTGGCAGTGG AAGAATTTCA GTGGACTCCA	540
1028		600
1029 1030	GGAGGTCCGC TCGCACGTGC CTAAGTTCGA TGCTACCTGG GCCACTGCTC GCGAGGTCAC	600
1030	TCTGAAGACT TTTGCTGAAG ATAACAGTGC CAGCGTGCAG GCCACTATGT ACAAGATGGC	660
1032		700
1033 1034	AGAGCAAATC CTGGCGCGCC AGCAGCTGAT CGAGACTGTC GAGTACTCGT TGCCTAACAA	720
1035	GCACTATTTC GAAATCGACC TGAGCTGGCA CAAGGGCCTC CAAAACACCG GCAAGAACGC	780
1036		040
1037 1038	CGAGGTCTTC GCTCCTCAGT CGGACCCCAA CGGTCTGATC AAGTGTACCG TCGGCCGGTC	840
1039	CTCTCTGAAG TCTAAATTGT AAACCAACAT GATTCTCACG TTCCGGAGTT TCCAAGGCAA	900
1040	ACTGTATATA GTCTGGGATA GGGTATAGCA TTCATTCACT TGTTTTTTAC TTCCAAAAAA	960
1041 1042	ACTGTATATA GTCTGGGATA GGGTATAGCA TTCATTCACT TGTTTTTTAC TTCCAAAAAA	900
1043	АААААААА ААААААААА ААААААААА ААААААААА	1013
1044	(2) INPODMARION FOR CRO ID NO. 21.	
1045 1046	(2) INFORMATION FOR SEQ ID NO:31:	
1047	(i) SEQUENCE CHARACTERISTICS:	
1048	(A) LENGTH: 207 base pairs	
1049	(B) TYPE: nucleic acid	
1050 1051	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
1051	(b) ToroLogi. Timear	
1053	(ii) MOLECULE TYPE: DNA (genomic)	
1054		
1055	(iii) HYPOTHETICAL: NO	
1056 1057		
1057	(vii) IMMEDIATE SOURCE:	
1059	(B) CLONE: Synthetic GAL7 fragment	
1060		
1061		
1062	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:	
1063 1064	CGCGTCTATA CTTCGGAGCA CTGTTGAGCG AAGGCTCATT AGATATATTT TCTGTCATTT	60
1065	COCCIOININ CITOCONCON CICITONCOC INCCCIONITI NOMINIMI I I I I I I I I I I I I I I I I I	
1066	TCCTTAACCC AAAAATAAGG GAGAGGGTCC AAAAAGCGCT CGGACAACTG TTGACCGTGA	120
1067	magallagana magaminana amammalali libarahan angalia amalikanin mamamilagan	180
1068 1069	TCCGAAGGAC TGGCTATACA GTGTTCACAA AATAGCCAAG CTGAAAATAA TGTGTAGCCT	100
1070	TTAGCTATGT TCAGTTAGTT TGGCATG	207
1071		

RAW SEQUENCE LISTING PATENT APPLICATION US/07/920,519

DATE: 09/22/93 TIME: 09:28:39

1073	1072	(2) INFORMATION FOR SEQ ID NO:32:	
(Å) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (D) TOPOLOGY: linear (E) MOLECULE TYPE: DNA (genomic) (II) MOLECULE TYPE: DNA (genomic) (III) MOLECULE DESCRIPTION: SEQ ID NO:32: (III) SEQUENCE DESCRIPTION: SEQ ID NO:32: (III) SEQUENCE CHARACTERISTICS: (III) SEQUENCE CHARACTERISTICS: (III) SEQUENCE CHARACTERISTICS: (III) MOLECULE TYPE: DNA (genomic) (II		(1) CECUENCE CUADACTEDISTICS.	
1076 (E) TYPE: nucleic acid 1077 (C) STRANDEDNESS: single 1079 1080 (ii) MOLECULE TYPE: DNA (genomic) 1081 1082 (iii) HYPOTHETICAL: NO 1083 1084 1085 (Vii) IMMEDIATE SOURCE: 1086 (E) CLONE: Modified XbaI-MluI adapter 1087 1088 1089 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32: 1090 1091 CTAGGCTAGC GGGCCCGCAT GCA 23 1092 1093 (2) INFORMATION FOR SEQ ID NO:33: 1094 1095 (i) SEQUENCE CHARACTERISTICS: 1096 (A) LENGTH: 422 base pairs 1097 (B) TYPE: nucleic acid 1099 (C) STRANDEDNESS: single 1099 (D) TOPOLOGY: linear 1100 1101 (ii) MOLECULE TYPE: DNA (genomic) 1102 (iii) HYPOTHETICAL: NO 1104 1105 (Vii) IMMEDIATE SOURCE: 1107 (B) CLONE: Plasmid pSE1 "site binding to HindIII" 1108 fragment 1110 1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1121 AGCTGGCTGC CATCTCCT TCACGGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 107 108 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGCTCTGAC CTGAGGCTGC CAGCCGCTTA 120 1211 GGTTACTGTT TCTGCGCCGT TACAACTTCA AGGTATGCGC TAGGGCCGG CAGCGCGGCAT 120 1211 GGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TAGGGCCGG CAGGCGGCAT 120 1211 GGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TAGGGCCGG CAGCGCGCAT 120 1211 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC CAGGCCGGCAT 120 1211 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TAGGGCCGG CAGGCGGCAT 120 1211 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TAGGGCCGG CAGGCGGCAT 120 1221 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TAGGGCCGG CAGGCGGCAT 120 121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TAGGGCCGGCAT 120 121 CGTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TAGGACCTGG CAGGCGGCAT 120 121 CGTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGACCTGG CAGGCGGCAT		\ - / -	
1077			
Optopology: linear Optopol		, ,	
1079			
1081		, ,	
1082	1080	(ii) MOLECULE TYPE: DNA (genomic)	
1083 1084 1085 1086 (Vii) IMMEDIATE SOURCE: 1086 (B) CLONE: Modified XbaI-MluI adapter 1087 1088 1089 (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:32: 1090 1091 CTAGGCTAGC GGGCCCGCAT GCA 23 1092 (2) INFORMATION FOR SEQ ID NO:33: 1094 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 422 base pairs 1097 (B) TYPE: nucleic acid 1098 (C) STRANDEDNESS: single 1099 (D) TOPOLOGY: linear 1100 1101 (ii) MOLECULE TYPE: DNA (genomic) 1102 1103 (iii) HYPOTHETICAL: NO 1104 1105 (Vii) IMMEDIATE SOURCE: 1107 1108			
1084		(iii) HYPOTHETICAL: NO	
1085			
1086 1087 1088 1089 1090 1091 1092 1092 1093 1094 1095 1096 1097 1097 1098 1099 1099 1099 1099 1099 1099 1090 1091 1091 1092 1093 1094 1095 1096 1097 1098 1098 1099 1099 1099 1099 1099 1099			
1087 1088 1089 1090 1091 1091 1092 1093 1093 1094 1095 1096 1097 1096 1098 1099 (a) LENGTH: 422 base pairs 1099 1099 1099 1090 1091 1090 1091 1090 1091 1000 1001 1001 1001 1001 1001 1001 1001 1001 1002 1003 1004 1005 1006 1006 1007 1007 1008 1008 1009 1009 1009 1009 1000 1001 1001			
1088 1089 1090 1091 1092 1092 1093 1093 (2) INFORMATION FOR SEQ ID NO:33: 1094 1095 (3) SEQUENCE CHARACTERISTICS: 1096 (A) LENGTH: 422 base pairs 1097 (B) TYPE: nucleic acid (C) STRANDEDNESS: single 1099 (D) TOPOLOGY: linear 1100 1101 (ii) MOLECULE TYPE: DNA (genomic) 1102 1103 ((iii) HYPOTHETICAL: NO 1104 1105 1106 ((vii) IMMEDIATE SOURCE: 1107 (B) CLONE: Plasmid pSE1 "site binding to HindIII" 1108 1109 1110 1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1113 AGCTGGCTCG CATCTCTCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 60 1114 115 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1119 1100 1111 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1119 1101 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCCT TACAACTTCA AGGTATGCGC TAGGGCCGC CAGGCCGCAT 300		(B) CLONE: Modified XDai-Miul adapter	
1089			
1090 1091 CTAGGCTAGC GGGCCCGCAT GCA 23 1092 1093 (2) INFORMATION FOR SEQ ID NO:33: 1094 (1) SEQUENCE CHARACTERISTICS: 1096 (A) LENGTH: 422 base pairs 1097 (B) TYPE: nucleic acid 1098 (C) STRANDEDNESS: single 1099 (D) TOPOLOGY: linear 1100 1101 (ii) MOLECULE TYPE: DNA (genomic) 1102 1103 (iii) HYPOTHETICAL: NO 1104 1105 1106 (vii) IMMEDIATE SOURCE: 1107 (B) CLONE: Plasmid pSE1 "site binding to HindIII" 1108 1110 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1113 AGCTGGCTCG CATCTCTCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 60 1114 115 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GTCTCCACG CTTTGCCTGA CCCTGCTTG TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TAGGCCGCAT 300		(vi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
1091 CTAGGCTAGC GGGCCCGCAT GCA 23 1092 1093 (2) INFORMATION FOR SEQ ID NO:33: 1094 1095 (3) SEQUENCE CHARACTERISTICS: 1096 (A) LENGTH: 422 base pairs 1097 (B) TYPE: nucleic acid 1098 (C) STRANDEDNESS: single 1099 (D) TOPOLOGY: linear 1100 1101 (ii) MOLECULE TYPE: DNA (genomic) 1102 1103 (iii) HYPOTHETICAL: NO 1104 1105 1106 (vii) IMMEDIATE SOURCE: 1107 (B) CLONE: Plasmid pSE1 "site binding to HindIII" 1108 fragment 1109 1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1111 1112 1113 AGCTGGCTCG CATCTCTCCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 1114 115 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGATCTCTA CTCTTTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGT TGGGACCTGC CAGGCGCAT 300		(XI) DECORACE DESCRIPTION. DEC 15 NO. 32.	
1092 1093 (2) INFORMATION FOR SEQ ID NO:33: 1094 1095 (i) SEQUENCE CHARACTERISTICS: 1096 (A) LENGTH: 422 base pairs 1097 (B) TYPE: nucleic acid 1098 (C) STRANDEDNESS: single 1099 (D) TOPOLOGY: linear 1100 1101 (ii) MOLECULE TYPE: DNA (genomic) 1102 1103 (iii) HYPOTHETICAL: NO 1104 1105 1106 (vii) IMMEDIATE SOURCE: 1107 (B) CLONE: Plasmid pSE1 "site binding to HindIII" 1108 fragment 1109 1110 1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1113 AGCTGGCTCG CATCTCTCT TCACGCGCCC GCCGCCTAC CTGAGGCCGC CATCCACGCC 60 1114 1115 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCTGATTGCTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGC CAGGCGGCAT 300		CTAGGCTAGC GGGCCCGCAT GCA	23
1094 1095 (i) SEQUENCE CHARACTERISTICS: 1096 (A) LENGTH: 422 base pairs 1097 (B) TYPE: nucleic acid 1098 (C) STRANDEDNESS: single 1099 (D) TOPOLOGY: linear 1100 1101 (ii) MOLECULE TYPE: DNA (genomic) 1102 1103 (iii) HYPOTHETICAL: NO 1104 1105 1106 (vii) IMMEDIATE SOURCE: 1107 (B) CLONE: Plasmid pSE1 "site binding to HindIII" 1108 fragment 1109 1110 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1113 AGCTGGCTCG CATCTCTCCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 60 1114 1115 GGTGAGTCGC GTTCTGCCGC CTCCCGCCTG TGGTGCCTCC TGAACTGCGT CCGCCGTCTA 120 1116 117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300			
1095 (i) SEQUENCE CHARACTERISTICS: 1096 (A) LENGTH: 422 base pairs 1097 (B) TYPE: nucleic acid 1098 (C) STRANDEDNESS: single 1099 (D) TOPOLOGY: linear 1100 1101 (ii) MOLECULE TYPE: DNA (genomic) 1102 1103 (iii) HYPOTHETICAL: NO 1104 1105 1106 (vii) IMMEDIATE SOURCE: 1107 (B) CLONE: Plasmid pSE1 "site binding to HindIII" 1108 fragment 1109 1110 1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1113 AGCTGGCTCG CATCTCTCT TCACGCGCCC GCCGCCTAC CTGAGGCCGC CATCCACGCC 60 1114 115 GGTGAGTCGC GTTCTGCCGC CTCCCGCCTG TGGTGCCTC TGAACTGCGT CCGCCGTCTA 120 1116 1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGGTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC CAGGCCGCAT 300		(2) INFORMATION FOR SEQ ID NO:33:	
1096 (A) LENGTH: 422 base pairs 1097 (B) TYPE: nucleic acid 1098 (C) STRANDEDNESS: single 1099 (D) TOPOLOGY: linear 1100 1101 (ii) MOLECULE TYPE: DNA (genomic) 1102 1103 (iii) HYPOTHETICAL: NO 1104 1105 1106 (vii) IMMEDIATE SOURCE: 1107 (B) CLONE: Plasmid pSE1 "site binding to HindIII" 1108 1110 1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1113 AGCTGGCTCG CATCTCTCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 60 1114 1115 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TAGGCCGCCAGGCCAT 300	1094		
1097 (B) TYPE: nucleic acid 1098 (C) STRANDEDNESS: single 1099 (D) TOPOLOGY: linear 1100 1101 (ii) MOLECULE TYPE: DNA (genomic) 1102 1103 (iii) HYPOTHETICAL: NO 1104 1105 1106 (vii) IMMEDIATE SOURCE: 1107 (B) CLONE: Plasmid pSE1 "site binding to HindIII" 1108 fragment 1109 1110 1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1113 AGCTGGCTCG CATCTCTCT TCACGCGCCC GCCGCCTAC CTGAGGCCGC CATCCACGCC 60 1114 1115 GGTAGGTCGC GTTCTGCCGC CTCCCGCCTG TGGTGCCTCC TGAACTGCGT CCGCCGTCTA 120 1116 1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300	1095	\ - / · · - 2 · - · · · - · · ·	
1098 (C) STRANDEDNESS: single 1099 (D) TOPOLOGY: linear 1100 1101 (ii) MOLECULE TYPE: DNA (genomic) 1102 1103 (iii) HYPOTHETICAL: NO 1104 1105 1106 (vii) IMMEDIATE SOURCE: 1107 (B) CLONE: Plasmid pSE1 "site binding to HindIII" 1108 fragment 1109 1110 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1113 AGCTGGCTCG CATCTCTCT TCACGCGCCC GCCGCCTAC CTGAGGCCGC CATCCACGCC 60 1114 1115 GGTGAGTCGC GTTCTGCCGC CTCCCGCCTG TGGTGCCTCC TGAACTGCGT CCGCCGTCTA 120 1116 1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300			
1099 (D) TOPOLOGY: linear 1100 1101 (ii) MOLECULE TYPE: DNA (genomic) 1102 1103 (iii) HYPOTHETICAL: NO 1104 1105 1106 (vii) IMMEDIATE SOURCE: 1107 (B) CLONE: Plasmid pSE1 "site binding to HindIII" 1108 fragment 1109 1110 1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1113 AGCTGGCTCG CATCTCTCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 60 1114 1115 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCCAC CTGAGCTCTA AACTTACCTA 120 1116 1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300			
1100 1101 (ii) MOLECULE TYPE: DNA (genomic) 1102 1103 (iii) HYPOTHETICAL: NO 1104 1105 1106 (vii) IMMEDIATE SOURCE: 1107 (B) CLONE: Plasmid pSE1 "site binding to HindIII" 1108 fragment 1109 1110 1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1113 AGCTGGCTCG CATCTCTCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 60 1114 1115 GGTAGGTCGC GTTCTGCCGC CTCCCGCCTG TGGTGCCTCC TGAACTGCGT CCGCCGTCTA 120 1116 1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300		· · · · · · · · · · · · · · · · · · ·	
1101 (ii) MOLECULE TYPE: DNA (genomic) 1102 1103 (iii) HYPOTHETICAL: NO 1104 1105 1106 (vii) IMMEDIATE SOURCE: 1107 (B) CLONE: Plasmid pSE1 "site binding to HindIII" 1108 fragment 1109 1110 1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1113 AGCTGGCTCG CATCTCTCCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 60 1114 1115 GGTAGGCTCC CATCTGCCGC CTCCCGCCTG TGGTGCCTCC TGAACTGCGT CCGCCGTCTA 120 1116 1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300		(D) TOPOLOGY: linear	
1102 1103 (iii) HYPOTHETICAL: NO 1104 1105 1106 (vii) IMMEDIATE SOURCE: 1107 (B) CLONE: Plasmid pSE1 "site binding to HindIII" 1108 fragment 1109 1110 1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1113 AGCTGGCTCG CATCTCTCCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 60 1114 1115 GGTGAGTCGC GTTCTGCCGC CTCCCGCCTG TGGTGCCTCC TGAACTGCGT CCGCCGTCTA 120 1116 1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300		(ii) MOLEGULE MUDE, DNA (gonomia)	
1103 (iii) HYPOTHETICAL: NO 1104 1105 1106 (vii) IMMEDIATE SOURCE: 1107 (B) CLONE: Plasmid pSE1 "site binding to HindIII" 1108 fragment 1109 1110 1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1113 AGCTGGCTCG CATCTCTCCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 60 1114 1115 GGTGAGTCGC GTTCTGCCGC CTCCCGCCTG TGGTGCCTCC TGAACTGCGT CCGCCGTCTA 120 1116 1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300		(II) MODECOLE TIPE: DNA (Genomic)	
1104 1105 1106 (vii) IMMEDIATE SOURCE: 1107 (B) CLONE: Plasmid pSE1 "site binding to HindIII" 1108 fragment 1109 1110 1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1113 AGCTGGCTCG CATCTCTCCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 60 1114 1115 GGTGAGTCGC GTTCTGCCGC CTCCCGCCTG TGGTGCCTCC TGAACTGCGT CCGCCGTCTA 120 1116 1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300		/iii HYDOTHETICAL: NO	
1105 1106 (vii) IMMEDIATE SOURCE: 1107 (B) CLONE: Plasmid pSE1 "site binding to HindIII" 1108 fragment 1109 1110 1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1113 AGCTGGCTCG CATCTCTCCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 60 1114 1115 GGTGAGTCGC GTTCTGCCGC CTCCCGCCTG TGGTGCCTCC TGAACTGCGT CCGCCGTCTA 120 1116 1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300		(III) MITOTRETICAD. NO	
1106 (vii) IMMEDIATE SOURCE: 1107 (B) CLONE: Plasmid pSE1 "site binding to HindIII" 1108 fragment 1109 1110 1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1113 AGCTGGCTCG CATCTCTCCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 60 1114 1115 GGTGAGTCGC GTTCTGCCGC CTCCCGCCTG TGGTGCCTCC TGAACTGCGT CCGCCGTCTA 120 1116 1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300			
1108 fragment 1109 1110 1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1113 AGCTGGCTCG CATCTCTCCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 60 1114 1115 GGTGAGTCGC GTTCTGCCGC CTCCCGCCTG TGGTGCCTCC TGAACTGCGT CCGCCGTCTA 120 1116 1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300		(vii) IMMEDIATE SOURCE:	
1110 1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1113 AGCTGGCTCG CATCTCTCCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 60 1114 1115 GGTGAGTCGC GTTCTGCCGC CTCCCGCCTG TGGTGCCTCC TGAACTGCGT CCGCCGTCTA 120 1116 1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300	1107	(B) CLONE: Plasmid pSE1 "site binding to HindIII"	
1110 1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1113 AGCTGGCTCG CATCTCTCCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 60 1114 1115 GGTGAGTCGC GTTCTGCCGC CTCCCGCCTG TGGTGCCTCC TGAACTGCGT CCGCCGTCTA 120 1116 1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300	1108	fragment	
1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: 1112 1113 AGCTGGCTCG CATCTCTCCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 60 1114 1115 GGTGAGTCGC GTTCTGCCGC CTCCCGCCTG TGGTGCCTCC TGAACTGCGT CCGCCGTCTA 120 1116 1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300			
1112 1113 AGCTGGCTCG CATCTCTCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 60 1114 1115 GGTGAGTCGC GTTCTGCCGC CTCCCGCCTG TGGTGCCTCC TGAACTGCGT CCGCCGTCTA 120 1116 1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300			
AGCTGGCTCG CATCTCTCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 60 1114 1115 GGTGAGTCGC GTTCTGCCGC CTCCCGCCTG TGGTGCCTCC TGAACTGCGT CCGCCGTCTA 120 1116 1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
1114 1115 GGTGAGTCGC GTTCTGCCGC CTCCCGCCTG TGGTGCCTCC TGAACTGCGT CCGCCGTCTA 120 1116 1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300			60
1115 GGTGAGTCGC GTTCTGCCGC CTCCCGCCTG TGGTGCCTCC TGAACTGCGT CCGCCGTCTA 120 1116 1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300		AGCTGGCTCG CATCTCTCCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC	80
1116 1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300		CATALLEROR CHICAGO CHOCOCCOCTA TARTACOCTO TALLETACOCT COGOCGTOTA	120
1117 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180 1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300		delenging diletenge cicedecia idaidecide idaneidedi codocaicia	-20
1118 1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300		GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA	180
1119 GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240 1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300			
1120 1121 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300		GACTCAGCCG GCTCTCCACG CTTTGCCTGA CCCTGCTTGC TCAACTCTAC GTCTTGTTT	240
1122	1121	CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT	300
	1122		

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1123	CTGGGACCCC TAGGAAGGC TTGGGGGTCC TCGTGCCCAA GGCAGGGAAC ATAGTGGTCC	360
1124 1125	CAGGAAGGGG AGCAGAGGCA TCAGGGTGTC CACTTTGTCT CCGCAGCTCC TGAGCCTGCA	420
1126 1127 1128	GA	422
1129 1130	(2) INFORMATION FOR SEQ ID NO:34:	
1131 1132 1133 1134 1135	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 77 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
1136 1137 1138	(ii) MOLECULE TYPE: DNA (genomic)	
1139 1140 1141	(iii) HYPOTHETICAL: NO	
1141 1142 1143 1144 1145	<pre>(vii) IMMEDIATE SOURCE: (B) CLONE: Synthetic HindIII-"site binding to BamHI"</pre>	
1146 1147 1148	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:	
1149 1150	AGCTTGTCGA CTAATACGAC TCACTATAGG GCGCCGCGG GCCCCTGCAG GAATTCGGAT	60
1151 1152	CCCCGGGTG ACTGACT	77
1153 1154	(2) INFORMATION FOR SEQ ID NO:35:	
1155 1156 1157 1158 1159 1160	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 61 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
1161 1162	(ii) MOLECULE TYPE: DNA (genomic)	
1163 1164 1165	(iii) HYPOTHETICAL: NO	
1166 1167 1168 1169	<pre>(vii) IMMEDIATE SOURCE: (B) CLONE: Synthetic HindIII-AccI fragment</pre>	
1170 1171	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:	
1172 1173	AGCTTGCCGC CACTATGTCC GCAGTAAAAG CAGCCCGCTA CGGCAAGGAC AATGTCCGCG	60

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1174	T	61
1175 1176	(2) INFORMATION FOR SEQ ID NO:36:	
1177 1178 1179 1180 1181 1182 1183	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 920 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
1184	(ii) MOLECULE TYPE: DNA (genomic)	
1185 1186 1187	(iii) HYPOTHETICAL: NO	
1188 1189 1190 1191 1192	<pre>(vii) IMMEDIATE SOURCE: (B) CLONE: HindIII-SnaBI fragment</pre>	
1193 1194	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:	
1195 1196	AGCTTGCCGC CACTATGTCC GCAGTAAAAG CAGCCCGCTA CGGCAAGGAC AATGTCCGCG	60
1197 1198	TCTACAAGGT TCACAAGGAC GAGAAGACCG GTGTCCAGAC GGTGTACGAG ATGACCGTCT	120
1199 1200	GTGTGCTTCT GGAGGGTGAG ATTGAGACCT CTTACACCAA GGCCGACAAC AGCGTCATTG	180
1201	TCGCAACCGA CTCCATTAAG AACACCATTT ACATCACCGC CAAGCAGAAC CCCGTTACTC	240
1202 1203	CTCCCGAGCT GTTCGGCTCC ATCCTGGGCA CACACTTCAT TGAGAAGTAC AACCACATCC	300
1204 1205	ATGCCGCTCA CGTCAACATT GTCTGCCACC GCTGGACCCG GATGGACATT GACGGCAAGC	360
1206 1207	CACACCCTCA CTCCTTCATC CGCGACAGCG AGGAGAAGCG GAATGTGCAG GTGGACGTGG	420
1208 1209	TCGAGGGCAA GGGCATCGAT ATCAAGTCGT CTCTGTCCGG CCTGACCGTG CTGAAGAGCA	480
1210 1211	CCAACTCGCA GTTCTGGGGC TTCCTGCGTG ACGAGTACAC CACACTTAAG GAGACCTGGG	540
1212 1213	ACCGTATCCT GAGCACCGAC GTCGATGCCA CTTGGCAGTG GAAGAATTTC AGTGGACTCC	600
1214 1215	AGGAGGTCCG CTCGCACGTG CCTAAGTTCG ATGCTACCTG GGCCACTGCT CGCGAGGTCA	660
1216 1217	CTCTGAAGAC TTTTGCTGAA GATAACAGTG CCAGCGTGCA GGCCACTATG TACAAGATGG	720
1218 1219	CAGAGCAAAT CCTGGCGCGC CAGCAGCTGA TCGAGACTGT CGAGTACTCG TTGCCTAACA	780
1220 1221	AGCACTATTT CGAAATCGAC CTGAGCTGGC ACAAGGGCCT CCAAAACACC GGCAAGAACG	840
1222 1223 1224	CCGAGGTCTT CGCTCCTCAG TCGGACCCCA ACGGTCTGAT CAAGTGTACC GTCGGCCGGT	900

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1225 CCTCTCTGAA GTCTAAATTG

1226

920

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/07/920,519

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(A) APPLICATION NUMBER: US/07/920,519

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SEQUENCE CORRECTION REPORT PATENT APPLICATION US/07/920,519

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